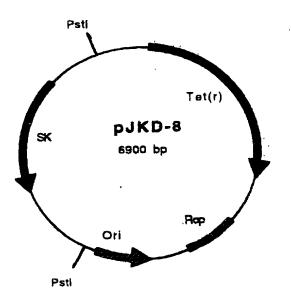
Fig. 1

(A) FBD(1,2) fused at the C-terminal of SK  SK	1	2	
(B) FBD(4,5) fused at the C-terminal of SK			<del>_</del>
SK	4	5	ال
		:	. [
(C) FBD(4,5) fused at the N-terminal of SK			
4 5 SK		•	-
			,
(D) FBD(4,5) fused at both the C as well as N-terminals of SK		•	
A 5 SK	4	5	٦

Fig. 2

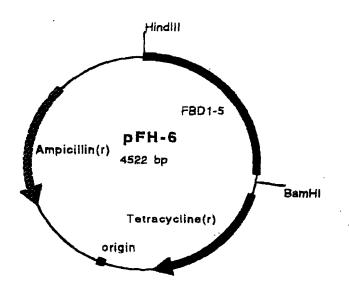


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31/11
1/1
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ile ala giy pro giu trp leu leu asp arg pro ser val asn asn ser gln leu val val
                                        91/31
AGC GIT CCT GCT ACT GIT GAG GGG ACG AAT CAA GAC ATT AGT CIT AAA TIT TIT GAA ATC
ser val ala gly thr val glu gly thr asm glm asp ile ser leu lys phe phe glu ile
                                        151/51
121/41
CAT CTA ACA TOA CGA. CCT GCT CAT GGA GGA AAG ACA GAG CAA GGC TTA AGT CCA AAA TCA
asp leu the ser arg pro ala his gly gly lys the glu gln gly leu ser pro lys ser
                                        211/71
AAA CCA TIT GCT ACT GAT AGT GGC GCG ATG TCA CAT AAA CIT GAG AAA GCT GAC TIA CTA
lys pro phe ala thr asp ser gly ala met ser his lys leu glu lys ala asp leu leu
                                        271/91
241/81
AAG GCT ATT CAA GAA CAA TIG ATC GCT AAC GTC CAC AGT AAC GAC GAC TAC TIT GAG GTC
lys als ile gin glu gln leu ile als asn val his ser asn asp asp tyr phe glu val
                                        331/111
301/101
ATT GAT TIT GCA AGC GAT GCA ACC AIT ACT GAT CGA AAC GGC AAG GTC TAC TIT GCT GAC
ile asp phe ala ser asp ala thr ile thr asp arg asn gly lys val tyr phe ala asp
                                        391/131
AAA GAT GGT TOG GTA ACC TTG CCG ACC CAA CCT GTC CAA GAA TTT TTG CTA AGC GGA CAT
lys aspigly ser val. thr heu pro thr gin pro val glu glu phe leu leu ser gly his
                                        451/151
421/141
GIG COC GIT AGA CCA TAT AAA GAA AAA CCA ATA CAA AAC CAA GCG AAA TCT GIT GAT GIG
val arg val arg pro tyr lys glu lys pro ile gln asn gln ala lys ser val asp val
                                         511/171
481/161
GAA TAT ACT GTA CAG TIT ACT CCC TTA AAC CCT GAT GAC GAT TTC AGA CCA GGT CTC AAA
glu tyr thr val gln phe thr pro leu asn pro asp asp phe arg pro gly leu lys
                                         571/191
541/181
GAT ACT AAG CTA TIG AAA ACA CTA GCT ATC GGT GAC ACC ATC ACA TCT CAA GAA TIA CTA
asp thr lys leu leu lys thr leu ala ile gly asp thr ile thr ser gln glu leu leu
                                         631/211
601/201
CCT CAA GCA CAA AGC ATT TTA AAC AAA AAC CAC CCA GGC TAT ACG ATT TAT GAA CGT GAC
ala gin ala gin ser ile leu asn lys asn his pro gly tyr thr ile tyr giu arg asp
                                         691/231
661/221
TOO TOA ATC GTE ACT CAT GAC AAT GAC ATT TTC CGT ACG ATT TTA CCA ATG CAT CAA GAG
ser ser ile val the his asp asn asp ile phe arg the ile leu pro met asp gln glu
                                         751/251
721/241
TIT ACT TAC COT GIT AMA AMT COG GAA CAM GCT TAT AGG ATC MAT AMA AMA TOT COT CTG
phe thr tyr arg val lys asn arg glu gln ala tyr arg ile asn lys lys ser gly leu
                                         811/271
 781/261
MAT CAN GAN ATA AAC AAC ACT GAC CTC ATC TCT GAG AAA TAT TAC GTC CTT AAA AAA GGG
ash glu glu ile ash ash thr asp leu ile ser glu lys tyr tyr val leu lys lys gly
                                         871/291
841/281
GAA AAG COG TAT GAT CCC TIT GAT CGC AGT CAC TIG AAA CIG TIC ACC AIC AAA TAC GIT
 glu lys pro tyr amp pro phe amp arg ser his leu lys leu phe thr ile lys tyr val
                                         931/311
901/301
 GAT GIT GAT ACC AAC GAA TIC CTA AAA AGT GAG CAG CIC TTA ACA GCT AGC GAA CGT AAC
 asp val asp thr.asn glu leu leu lys ser glu gln leu leu thr ala ser glu arg asn
                                         991/331
 961/321
 TTA CAC TTC ACA CAT TTA TAC GAT CCT CCT GAT AAG GCT AAA CTA CTC TAC AAC AAT CTC
 lou asp phe arg amp leu tyr asp pro arg asp lys ala lys leu leu tyr asn asn leu
                                         1051/351
 1021/341
 CAT GCT TIT GGT ATT ATG GAC TAT ACC TTA ACT GGA AAA GTA GAG GAT AAT CAC GAT GAC
 asp ala phe gly ile met asp tyr thr leu thr gly lys val glu asp asn his asp asp
                                         1111/371
 1081/361
 ACC AAC CGT ATC ATA ACC GTT TAT ATG GGC AAG CGA CCC GAA GGA GAG AAT GCT AGC TAT
 thr asn arg ile ile thr val tyr met gly lys arg pro glu gly glu asn ala ser tyr
                                         1171/391
 1141/381
 CAT TTA GCC TAT GAT AAA GAT CGT TAT ACC GAA GAA GAA CGA GAA GTT TAC ACC TAC CTG
 his leu ala tyr asp lys asp arg tyr thr glu glu glu arg glu val tyr ser tyr leu
                                         1231/411
 COT THE ACA GOG ACA COT ATA COT GAT AAC COT AAC GAC AAA TAA
 arg tyr thr gly thr pro the pro asp asn pro asn asp lys OCH
```

```
694 Spl I
                                                                    678 Msl I
                                                     533 BsmA !
                                                     532 Eco31 i
                                                     528 SexA
                                     417 Nsp I
417 BepLU11 I
417 BepLU11 I
372 Bel II
                                                                    675 BapH I
           118 Cla l
                                                                  680 BseR1
  94 PshA I
87 TI( I
37 Hind II
                                                                  658 Ple I
                                                                633 Sec I
                         256 Mie I
                                        408 Esp |
                                                              618 Aha III
                                                                                         876 Xmn I
                                                                                                           1051 Bsr I
                                                                                                                   1128 Bam I
1153 Baab I
             165 Afili
136 BsiY i
                               346 Acc |
310 Mwo |
                                                                                                  986 Bsi I
966 Eco57 I
7 Ava II
                                                     527 Tih1111
                                                                                   818 Ssp !
7 Asul
                                                 489 Bsp1407 l
                                                                            749 HinD III
              SK.DNA
                                                    1245 base pairs
                                                                                Unique Sites
```

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Fig. 5

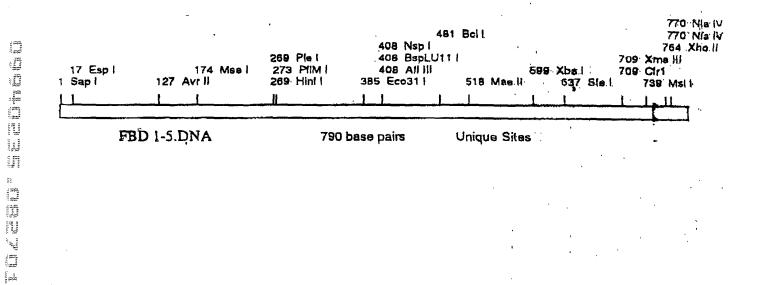


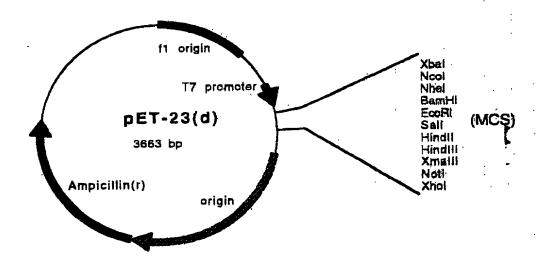
1/1	~	31/11 .	
		cce ete ect ete act	- · · · · · · · · · · · · · · · · · · ·
gln ala gln gln mer	val gln pro gln ser	pro val ala val ser	gin ser lys pro gly
61/21		91/31	
	•	AAT CAA CAG 10G GAC	
cys tyr asp asn gly	lys his tyr gln ile	asn gln gln trp glu	arg thr tyr leu gly
121/41		151/51	
aat cic tig git tgt .	ACT TOT TAT GGA GGA	AGC EGA GCT TTT AAC	TGC GAA AGT AAA CCT
asn val leu val cys	thr cha thr did did	ser arg gly phe asn	cys glu ser lys pro
181/61		21,1/71	
		act GGG AAC ACT TAC	
glu ala glu glu thr	cha bue seb la the	thr gly asn thr tyr	arg val gly asp thr
241/81		271/91	
		GAC TGT ACC TGC ATC	
	asp ser met ile trp	asp cys thr cys ile	gly ala gly arg gly
301/101	_	331/111	
		CAT GAA GGG GGT CAG	
	ile ala asn arg cys	pre and and and and	ser tyr lys ile gly
361/121		391/131	
			TET GIG TET CIT GGT
	pro his glu thr gly	gly tyr met leu glu	cha nat cha len all
421/141		451/151	
AAT GUA AAA GUA GAA	TIGG ACC TIGC AAG CCC	ATA GCT GAG AAG TGT	TIT GAT CAT GCT GCT
asm gry rys gry gru	erb cur cha The bro	ile ala glu lys cys	phe asp his ala ala
	CTT CC1 C11 100 B00	511/171	
als the act timesals	GIC GGA GAA ACG TOG	GAG AAG CCC TAC CAA	GGC TGG ATG ATG GTA
S41/181	Agr dia die cut tib	glu lys pro tyr gln	dry cub mer mer war
	CGA CAA CCC ACC CCA	571/191 CGC ATC ACT TGC ACT	
asp ove thr ove len	alv alu alv ser alv	arg ile thr cys thr	TCT, AGA AAT AGA TGC
601/201	Art Art Art per Ark	631/211	ser arg asn arg cys
	AGG ACA TOO TAT AGA	ATT GGA GAC ACC TGG	200 520 220 cam 220
asn asp oln asp thr	are the ser tyr are	the div asp the tro	ser lys lys asp asn
661/221		691/231	mer ria ria cah dau '
	CAG TGC ATC TGC ACA	GOC AAC GGC CGA GGA	GAG TOS ALG TOT CAG
arg gly asn leu leu	glm cvs ile cvs thr	gly asn gly arg gly	alu tra lue cue alu
721/241		751/251	
AGE CAC ACC TOT GTG	CAG ACC ACA TOG AGC	GGA TOT GGC CCC TTC	ACC GAT GIT CGT
arg his thr ser val	gln thr thr ser ser	gly ser gly pro phe	thr asp val arg

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in 1;\*

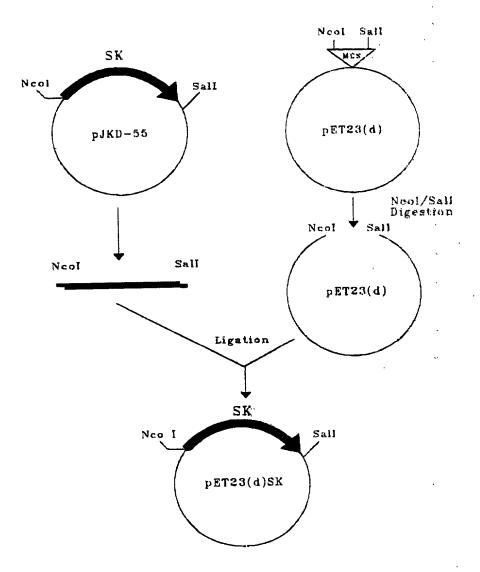
Fig. 7

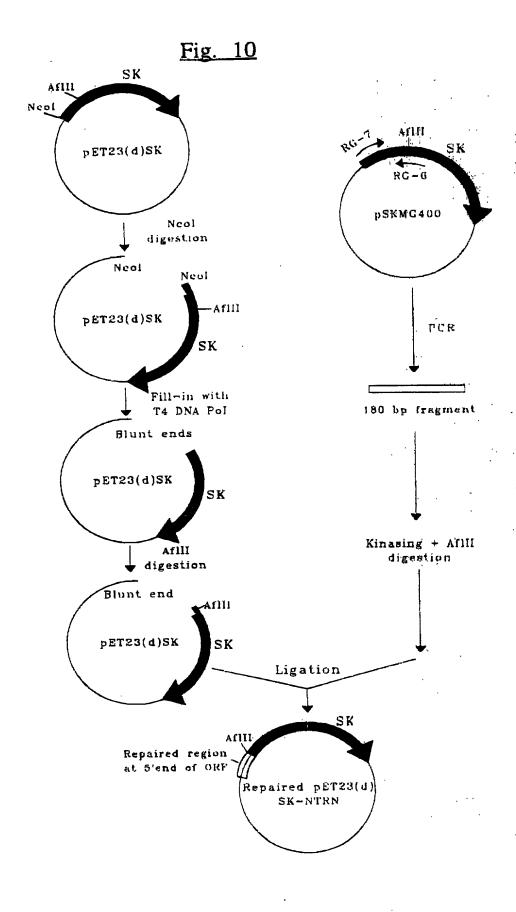




ngathza, maryna

Fig. 9





+ Z					
	. 10	20	30	40:	
	GCACCCGTGG	CCAGGACCCA	ACGCTGCCCG	AGATCTCGAT	CCCGCGAAAT
51	TAATACGACT	CACTATAGGG	AGACCACAAC	GGTTTCCCTC	TAGAAATAAT
101	TTTGTTTAAC	TTTAAGAAGG	AGATATACCA	TGATTGCTGG	ACCTGAGTGG
151	CTGCTAGACC	GTCCATCTGT	CAACAACAGC	CAATTGGTTG	TTAGCGTTGC
201	TGGTACTGTT	GAGGGGACGA	ATCAAGACAT	TAGTCTTAAA	TTTTTGAAA
251	TCGATCTAAC	ATCACGACCT	GCTCATGGAG	GAAAGACAGA	GCAAGGCTTA
301	AGTCCAAAAT	CAAAACCATT	TGCTACTGAT	AGTGGCGCGA	TGTCACATAA
351	ACTTGAGAAA	GCTGACTTAC	TAAAGGCTAT	TCAAGAACAA	TTGATCGCTA
401	ACGTCCACAG	TAACGACGAC	TACTTTGAGG	TCATTGATTT	TGCAAGCGAT
451	GCAACCATTA	CTGATCGAAA	CGGCAAGGTC	TACTTTGCTG	ACAAAGATGG
50]	TTCGGTAACC	TTGCCGACCC	AACCTGTCCA	AGAATTITIG .	CTAAGCGGAC
551	ATGTGCGCGT	TAGACCATAT	AAAGAAAAAC	CAATACAAAA	CCAAGCGAAA
601	TCTGTTGATG	TGGAATATAC	TGTACAGTTT	ACTCCCTTAA	ACCCTGATGA
651	CGATTTCAGA	CCAGGTCTCA	AAGATACTAA	GCTATTGAAA	ACACTAGCTA
701	TCGGTGACAC	CATCACATCT	CAAGAATTAC	TAGCTCAAGC	ACAAAGCATT
751	TTAAACAAAA	ACCACCCAGG	CTATACGATT	TATGAACGTG	ACTECTEAAT
801	CGTCACTCAT	GACAATGACA	TTTTCCGTAC	GATTTTACCA	ATGGATCAAG
851	AGTTTACTTA	CCGTGTTAAA	AATCGGGAAC	AAGCTTATAG	GATCAATAAA
901	AAATCTGGTC	TGAATGAAGA	AATAAACAAC	ACTGACCTGA	TCTCTGAGAA
951	ATATTACGTC	CTTAAAAAAG	GGGAAAAGCC	GTATGATCCC	TTTGATCGCA
1001	GTCACTTGAA	ACTGTTCACC	ATCAAATACG	TTGATGTCGA	TACCAACGAA
1051	TTGCTAAAAA	GTGAGCAGCT	CTTAACAGCT	AGCGAACGTA	ACTTAGACTT
1101	CAGAGATITA	TACGATCCTC	GTGATAAGGC	TAAACTACTC	TACAACAATC
1151	TCGATGCTTT	TGGTATTATG	GACTATACCT	TAACTGGAAA	AGTAGAGGAT
1201	AATCACGATG	ACACCAACCG	TATCATAACC	GTTTATATGG	GCAAGCGACC
1251	CGAAGGAGAG	AATGCTAGCT	ATCATTTAGC	CTATGATAAA	GATCGITATA
1301	CCGAAGAAGA	ACGAGAAGTT	TACAGCTACC	TGCGTTATAC	AGGGACACCT
1351	ATACCTGATA	ACCCTAACGA	CAAATAA		

Fig. 12

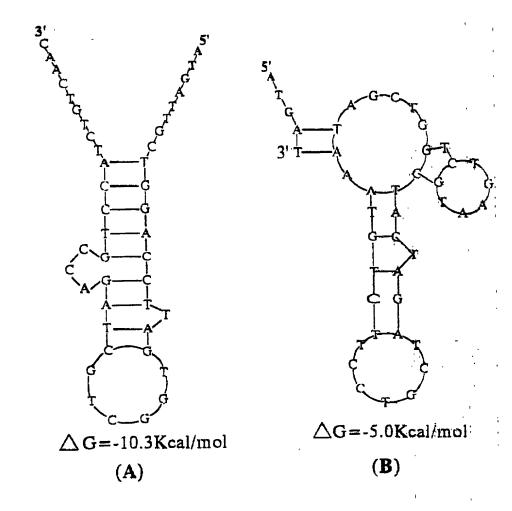
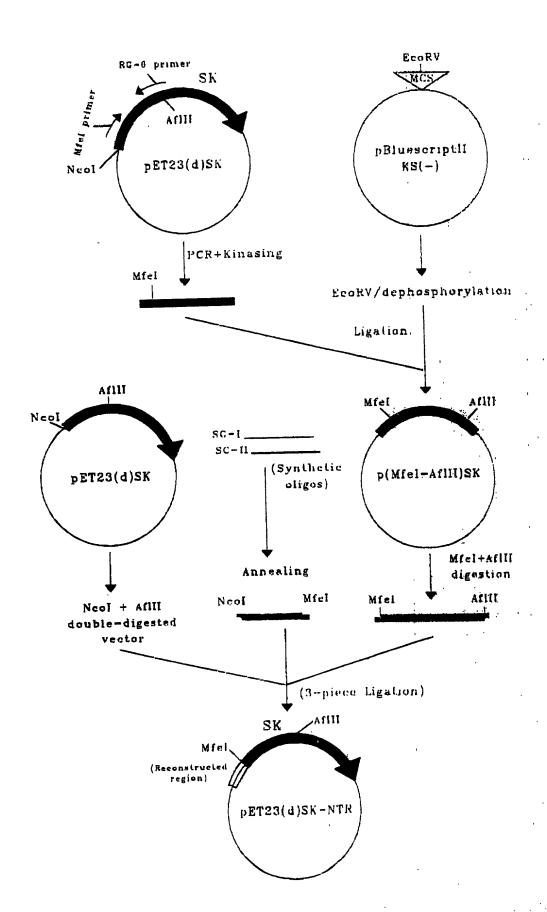
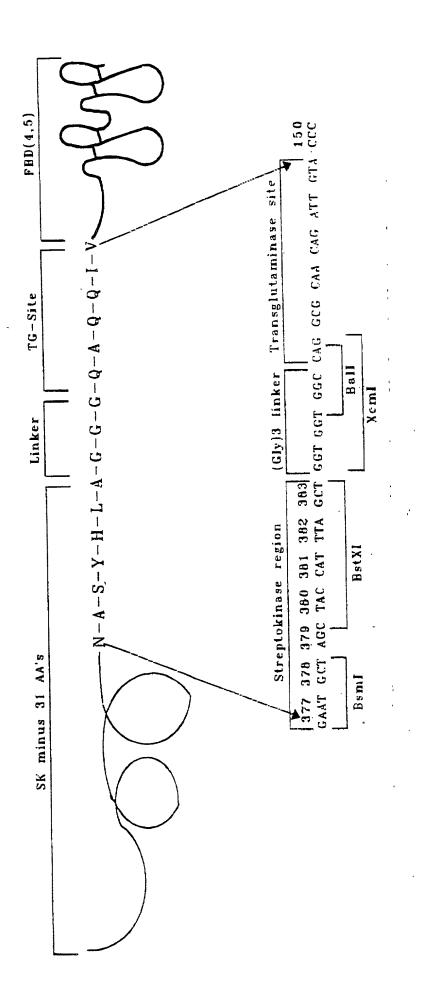


Fig. 13



	10	20	30	40.	'50
	TAATACGACT	CACTATAGGG	AGACCACAAC	GGTTTCCCTC	TAGAAATAAT
51	TTTGTTTAAC	TTTAAGAAGG	AGATATACCA	TGATAGCTGG.	TCCTGAATGG
101	CTACTAGATC	GTCCTTCTGT	AAATAACAGC	CAATTGGTTG	TTAGCGTT:GC
151	TGGTACTGTT	GAGGGGACGA	ATCAAGACAT	TAGTCTTAAA	TTTTTTGAAA
201	TCGATCTAAC	ATCACGACCT	GCTCATGGAG	GAAAGACAGA	GCAAGGCTTA
251	AGTCCAAAAT	CAAAACCATT	TGCTACTGAT	AGTGGCGCGA	TOTCACATAA
301	ACTTGAGAAA	GCTGACTTAC	TAAAGGCTAT	TCAAGAACAA	TTGATCGCTA
351	ACGTCCACAG	TAACGACGAC	TACTTTGAGG	TCATTGATTT	TGCAAGCGAT
401	GCAACCATTA	CTGATCGAAA	CGGCAAGGTC	TACTTTGCTG	ACAAAGATGG
451	TTCGGTAACC	TTGCCGACCC	AACCTGTCCA	AGAATITTTG	CTAAGCGGAC
501	ATGTGCGCGT	TAGACCATAT	AAAGAAAAAC	CAATACAAAA	CCAAGCGAAA
551	TCTGTTGATG	TGGAATATAC	TGTACAGTTT	ACTCCCTTAA	ACCCTGATGA
601	CGATTTCAGA	CCAGGTCTCA	AAGATACTAA	GCTATTGAAA	ACACTAGCTA
651	TCGGTGACAC	CATCACATCT	CAAGAATTAC	TAGCTCAAGC	ACAAAGCATT
701	TTAAACAAAA	ACCACCCAGG	CTATACGATT	TAT GAACGTG	ACTCCTCAAT
751	CGTCACTCAT	GACAATGACA	TTT TCCGTAC	GATTTTACCA	ATGGATCAAG
801	AGTTTACTTA	CCGTGTTAAA	AATCGGGAAC	AAGCTTATAG	GATCAATAAA'
851	AAATCTGGTC	TGAATGAAGA	AATAAACAAC	ACTGACCTGA	TCTCTGAGAA
901	ATATTACGTC	CTTAAAAAAG	GGGAAAAGCC	GTATGATCCC	TTTGATCGCA
951	GTCACTTGAA	ACTGTTCACC	ATCAAATACG	TTGATGTCGA	TACCAACGAA
1001	TTGCTAAAAA	GTGAGCAGCT	CTTAACAGCT	AGCGAACGTA	ACTTAGACTT
1051	CAGAGATTTA	TACGATCCTC	GTGATAAGGC	TAAACTACTC	TACAACAATC
1101	TCGATGCTTT	TGGTATTATG	GACTATACCT	TAACTGGAAA	AGTAGAGGAT
1151	AATCACGATG	ACACCAACCG	TATCATAACC	GTTTATATGG	GCAAGCGACC
1201	CGAAGGAGAG		ATCATTTAGC	CTATGATAAA	GATCGTTATA
1251	CCGAAGAAGA		TACAGCTACC	TGCGTTATAC	AGGGACACCT
1301	ATACCTGATA	ACCCTAACGA	CAAATAA		

Fig. 15



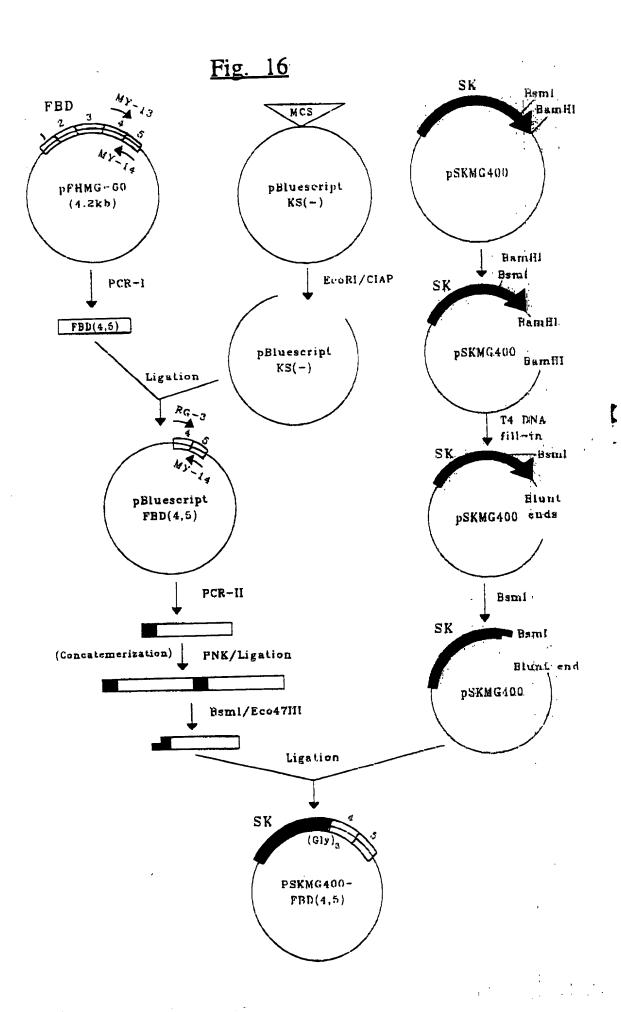
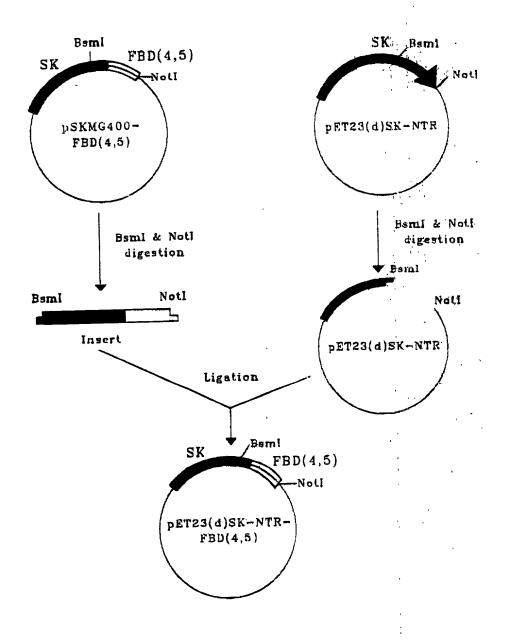


Fig. 17a



# Fig. 17b

	10	20	30	, 40	50
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5)	CTACTAGATC	GTCCTTCTGT	AAATAACAGC	CAATTGGTTG	TTAGCGTTGC
101	TGGTACTGTT	GAGGGGACGA	ATCAAGACAT	TAGTCTTAAA	TTTTTTGAAA
151	TCGATCTAAC	ATCACGACCT	GCTCATGGAG	GAAAGACAGA	GCAAGGCTTA
201	AGTCCAAAAT	CAAAACCATT	TGCTACTGAT	AGTGGCGCGA	TGTCACATAA
251	ACTTGAGAAA	GCTGACTTAC	TAAAGGCTAT	TCAAGAACAA	TTGATCGCTA-
301	ACGTCCACAG	TAACGACGAC	TACTTTGAGG	TCATTGATIT	TGCAAGCGAT
351	GCAACCATTA	CTGATCGAAA	CGGCAAGGTC	TACTTTGCTG	ACAAAGATGG
401	TTCGGTAACC	TTGCCGACCC	AACCTGTCCA	AGAATTTTTG	CTAAGCGGAC
451	ATGTGCGCGT	TAGACCATAT	AAAGAAAAAC	CAATACAAAA	CCAAGCGAAA
501	TCTGTTGATG	TGGAATATAC	TGTACAGTTT	ACTCCCTTAA	ACCCTGATGA
551	CGATTTCAGA	CCAGGTCTCA	AAGATACTAA	GCTATTGAAA	ACACTAGETA
601	TCGGTGACAC	CATCACATCT	CAAGAATTAC	TAGCTCAAGC	ACAAAGCATT
651	TTAAACAAAA	ACCACCCAGG	CTATACGATT	TAT GAACGTG	ACTCCTCAAT
701	CGTCACTCAT	GACAATGACA	TITTCCGTAC	GATTTTACCA	ATGGATCAAG
751	AGTTTACTTA	CCGTGTTAAA	AATCGGGAAC	AAGCTTATAG	GATCAATAAA
801	AAATCTGGTC	TGAATGAAGA	AATAAACAAC	ACTGACCTGA	TCTCTGAGAA
851	ATATTACGTC	CTTAAAAAAG	GGGAAAAGCC	GTATGATCCC	TTTGATCGCA
901	GTCACTTGAA	ACTGTTCACC	ATCAAATACG	TTGATGTCGA	TACCAACGAA
. 951	TTGCTAAAAA	GTGAGCAGCT	CTTAACAGCT	AGCGAACGTA	ACTTAGACTT
1001	CAGAGATTTA	TACGATCCTC	GTGATAAGGC	TAAACTACTC	TACAACAATC
1051	TCGATGCTTT	TGGTATTATG	GACTATACCT	TAACTGGAAA	AGTAGAGGAT
1101	AATCACGATG	ACACCAACCG	TAT CATAACC	GTTTATATGG	GCAAGCGAGC
1151	CGAAGGAGAG	AATGCTAGCT	ACCATTTAGC	TGGTGGTGGC	CAGGCGCAAC
1201	AGATTGTACC	CATAGCTGAG	AAGTGTTTTG	ATCATGCTGC	TGGGACTTCC
1251	TATGTGGTCG	GAGAAACGTG	GGAGAAGCCC	TACCAAGGCT	GGATGATGGT
1301	AGATTGTACT	TGCCTGGGAG	AAGGCAGCGG	ACGCATCACT	TGCACTTCTA
1351	GAAATAGATG	CAACGATCAG	GACACAAGGA	CATCCTATAG	AATTGGAGAC
1401	ACCTGGAGCA	AGAAGGATAA	TCGAGGAAAC	CTGCTCCAGT	GCATCTGCAC
1451	AGGCAACGGC	CGAGGAGAGT	GGAAGTGTGA	GAGGCACACC	TCTGTGCAGA
1501	CCACATCGAG	CGGATCTGGC	CCCTTCACCG	ATGTTCGTTA	G

Fig. 18

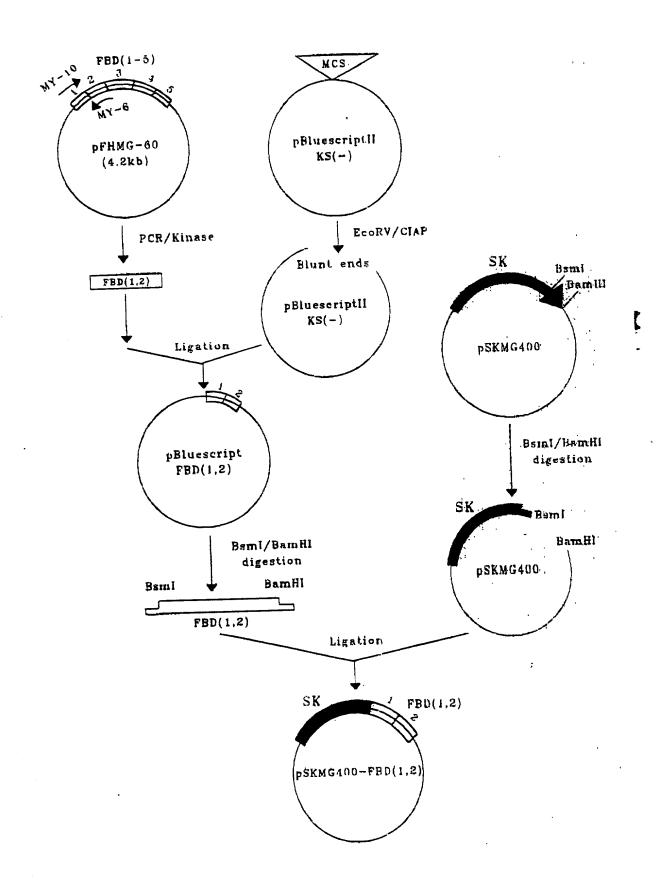
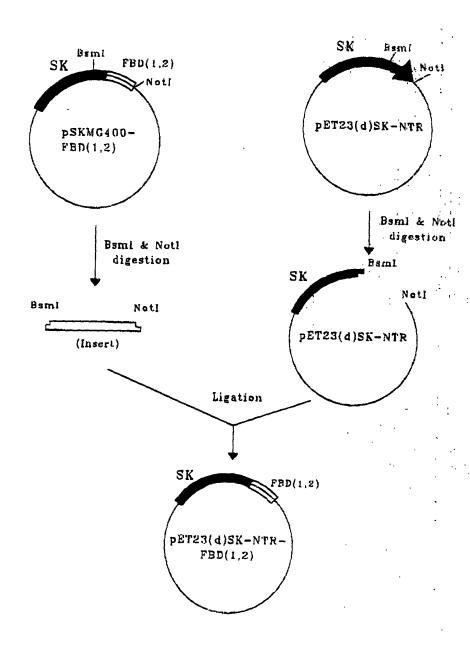


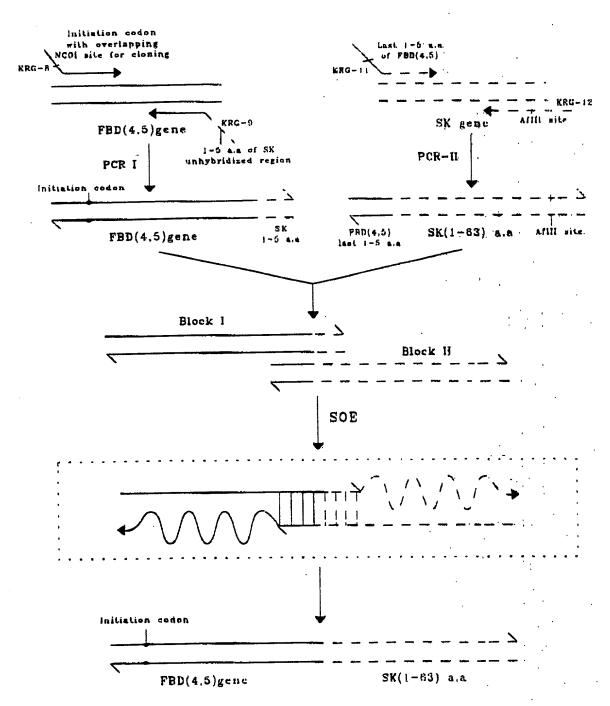
Fig. 19a



#### Fig. 19b

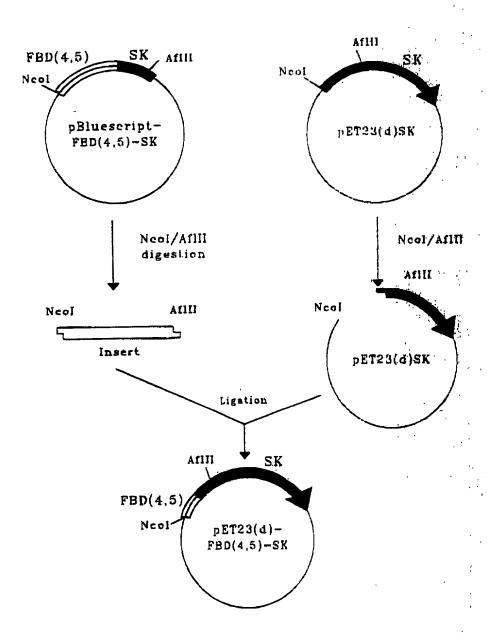
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51	GCACCCGTGG	CCAGGACCCA	ACGCTGCCCG	AGATCTCGAT	CCCGCGAAAT
101	TAATACGACT	CACTATAGGG	AGACCACAAC	GGTTTCCCTC	TAGAAATAAT
151	TITGTTTAAC	TTTAAGAAGG	AGATATACCA	TGATTGCTGG	ACCTGAGTGG
201	CTGCTAGACC	GTCCATCTGT	CAACAACAGC	CAATTGGTTG	TTAGCGTTGC
251	TGGTACTGTT	GAGGGGACGA	ATCAAGACAT	TAGTCTTAAA	TTTTTTGAAA
301	TCGATCTAAC	ATCACGACCT	GCTCATGGAG	GAAAGACAGA	GCAAGGCTTA
351	AGTCCAAAAT	CAAAACCATT	TGCTACTGAT	AGTGGCGCGA.	TGTCACATAA
401	ACTTGAGAAA	GCTGACTTAC	TAAAGGCTAT	TCAAGAACAA	TTGATCGCTA
451	ACGTCCACAG	TAACGACGAC	TACTTTGAGG	TCATTGATTT	TGCAAGCGAT
501	GCAACCATTA	CTGATCGAAA	CGGCAAGGTC	TACTTTGCTG	ACAAAGATGG
551	TTCGGTAACC	TTGCCGACCC	AACCTGTCCA	AGAATTITTG	CTAAGCGGAC
601	ATGTGCGCGT	TAGACCATAT	AAAGAAAAAC	CAATACAAAA	CCAAGCGAAA
651	TCTGTTGATG	TGGAATATAC	TGTACAGTTT	ACTCCCTTAA	ACCCTGATGA
701	CGATTTCAGA	CCAGGTCTCA	AAGATACTAA	GCTATTGAAA	ACACTAGCTA
751	TCGGTGACAC	CATCACATCT	CAAGAATTAC	TAGCTCAAGC	ACAAAGCATT
801	TTAAACAAAA	ACCACCCAGG	CTATACGATT	TATGAACGTG	ACTCCTCAAT
851	CGTCACTCAT	GACAATGACA	TTTTCCGTAC	GATTTTACCA	ATGGATCAAG
901	AGTITACTIA	CCGTGTTAAA	AATCGGGAAC	AAGCTTATAG	GATCAATAAA
951	AAATCTGGTC	TGAATGAAGA	AATAAACAAC	ACTGACCTGA	TCTCTGAGAA
1001	ATATTACGTC	CTTAAAAAAG	GGGAAAAGCC	GTATGATCCC	TTTGATCGCA
1051	GTCACTTGAA	ACTGTTCACC	ATCAAATACG	TTGATGTCGA	TACCAACGAA
1101	TTGCTAAAAA	GTGAGCAGCT	CTTAACAGCT	AGCGAACGTA.	ACTTAGACTT
1151	CAGAGATTTA	TACGATCCTC	GTGATAAGGC	TAAACTACTC	TACAACAATC
1201	TCGATGCTTT	TGGTATTATG	GACTATACCT	TAACTGGAAA	AGTAGAGGAT
1251	AATCACGATG	ACACCAACCG	TATCATAACC	GTTTATATGG	GCAAGCGACC
1301	CGAAGGAGAG	AATGCTAGCT	ATCATTTAGC	CGGTGGTGGT	CAGGCGCAGC
1351	AAATGGTTCA	GCCCCAGTCC	CCGGTGGCTG	TCAGTCAAAG	CAAGCCCGGT
1401	TGTTATGACA	ATGGAAAACA	CTATCAGATA	AATCAACAGT	GGGAGCGGAC
1451	CTACCTAGGT	AATGTGTTGG	TTTGTACTTG	TTATGGAGGA	AGCCGAGGTT
1501	TTAACTGCGA	AAGTAAACCT	GAAGCTGAAG	AGACTTGCTT	TGACAAGTAC
1551	ACTGGGAACA	CTTACCGAGT	GGGTGACACT	TATGAGCGTC	CTAAAGACTC
1601	CATGATCTGG	GACTGTACCT	GCATCGGGGC	TGGGCGAGGG	AGAATAAGCT
1651	GTACCATCTA	A			

Fig. 20



Recombinant Product

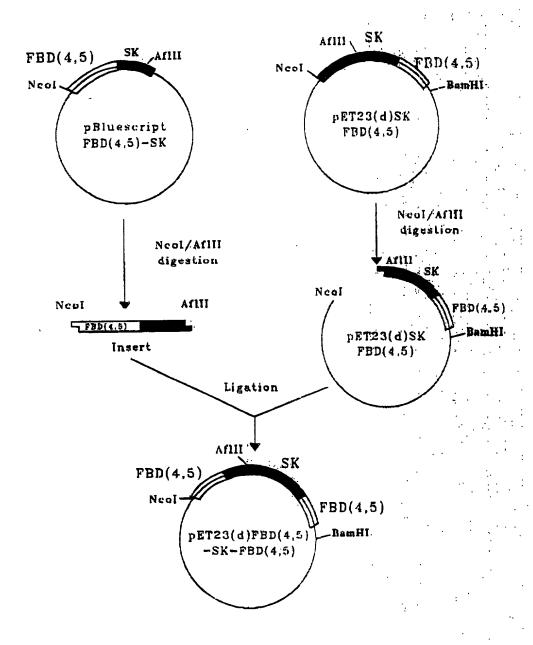
Fig. 21a



## Fig. 21b

				1	•
	10	20	30	40	50
1	TCGCTTCACG	TTCGCTCGCG	TATCGGTGAT	TCATTCTGCT	AACCAGTAAG
51	GCAACCCCGC	CAGCCTAGCC	GGGTCCTCAA	CGACAGGAGC	ACGATCATGC
101	GCACCCGTGG	CCAGGACCCA	ACGCTGCCCG	AGATCTCGAT	CCCGCGAAAT
151	TAATACGACT	CACTATAGGG	AGACCACAAC	GGTTTCCCTC	TAGAAATAAT
201	TTTGTTTAAC	TTTAAGAAGG	AGATATACEA	TGGTGCAAGC '	ACAACAGATT
251	GTACCCATAG	CTGAGAAGTG	TTTTGATCAT	GCTGCTGGGA	CTTCCTATGT
301	GGTCGGAGAA	ACGTGGGAGA	AGGCAGCGGA	CGCATCACTT	GCACTTCTAG
351	AAATAGATGC	AACGATCAGG	ACACAAGGAC	ATCCTATAGA	ATTGGAGACA
401	CCTGGAGCAA	GAAGGATAAT	CGAGGAAACC	TGCTCCAGTG	CATCTGCACA
451	GGCAACGGCC	GAGGAGAGTG	GAAGTGTGAG	AGGCACACCT.	CTGTGCAGAC
501	CACATCGAGC	GGATCTGGCC	CCTTCACCGA	TGTTCGTATT	GCTGGACCTG
551	AGTGGCTGCT	AGACCGTCCA	TCTGTCAACA	ACAGCCAATT	GGTTGTTAGC
601	GTTGCTGGTA	CTGTTGAGGG	GACGAAT.CAA	GACATTAGTC	TTAAATTTTT
651	TGAAATCGAT	CTAACATCAC	GACCTGCTCA	TGGAGGAAAG.	ACAGAGCAAG
701	GCTTAAGTCC	AAAATCAAAA	CCATTTGCTA	CTGATAGTGG	CGCGATGTCA
751	CATAAACTTG	AGAAAGCTGA	CTTACTAAAG	GCTATTCAAG	AACAATTGAT
801	CGCTAACGTC	CACAGTAACG	ACGACTACTT	TGAGGTCATT	GATTITGCAA
851	GCGATGCAAC	CATTACTGAT	CGAAACGGCA	AGGTCTACTT	TGCTGACAAA
901	GATGGTTCGG	TAACCTTGCC	GACCCAACCT	GTCCAAGAAT	TTTTGCTAAG
951	CGGACATGTG	CGCGTTAGAC	CATATAAAGA	AAAACCAATA	CAAAACCAAG
1001	CGAAATCTGT	TGATGTGGAA	TATACTGTAC	AGITTACTCC	CTTAAACCCT
1051	GATGACGATT	TCAGACCAGG	TCTCAAAGAT	ACTAAGCTAT	TGAAAACACT
1101	AGCTATCGGT	GACACCATCA	CATCTCAAGA	ATTACTAGET	CAAGCACAAA
1151	GCATTTTAAA	CAAAAACCAC	CCAGGCTATA	CGATTTATGA	ACGTGACTCC
1201	TCAATCGTCA	CTCATGACAA	TGACATTITC	CGTACGATTT	TACCAATGGA
1251	TCAAGAGTTT	ACTTACCGTG	TTAAAAATCG	GGAACAAGCT	TATAGGATCA
1301	ATAAAAAATC	TGGTCTGAAT	GAAGAAATAA	ACAACACTGA	CCTGATCTCT
1351	GAGAAATATT	ACGTCCTTAA	AAAAGGGGAA	AAGCCGTATG	ATCCCTTTGA.
1401	TCGCAGTCAC	TTGAAACTGT	TCACCATCAA	ATACGTTGAT	GTCGATACCA
1451	ACGAATTGCT	AAAAAGTGAG	CAGCTCTTAA	CAGCTAGCGA	ACGTAACTTA
1501	GACTTCAGAG	ATITATACGA	TCCTCGTGAT	AAGGCTAAAC	TACTCTACAA
1551	CAATCTCGAT	GCTTTTGGTA	TTATGGACTA	TACCTTAACT	GGAAAAGTAG
1601	AGGATAATÇA	CGATGACACC	AACCGTATCA	TAACCGTTTA	TATGGGCAAG
1651	CGACCCGAAG	GAGAGAATGC	TAGCTATCAT	TTAGCCTATG	ATAAAGATCO
1701	TTATACCGAA	GAAGAACGAG	AAGTTTACAG	CTACCTGCGT	TATACAGGGA
1751	CACCTATACC	TGATAACCCT	AACGACAAAT	AA ·	•

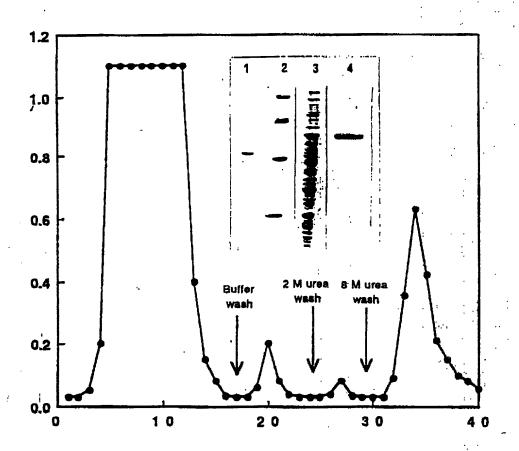
Fig. 22a



# Fig. 22b

	10	20	30	40	50
1	CGAAGACCAT	TCATGTTGTT	GCTCAGGTCG	CAGACGTTTT 1	GCAGCAGCAG
51	TCGCTTCACG	TTCGCTCGCG	TATCGGTGAT	TCATTCTGCT	AACCAGTAAG
101	GCAACCCCGC	CAGCCTAGCC	GGGTCCTCAA	CGACAGGAGC:	ACGATCATGC
151	GCACCCGTGG	CCAGGACCCA	ACGCTGCCCG	AGATCTCGAT	CCCGCGAAAT
201	TAATACGACT	CACTATAGGG	AGACCACAAC	GGTTTCCCTC ::	TAGAAATAAT
251	TITGTTTAAC	TTTAAGAAGG	AGATATACCA	'TGGTGCAAGC:	ACAACAGATT
301	GTACCCATAG	CTGAGAAGTG	TTTTGATCAT	GCTGCTGGGA	CTTCCTATGT
351	GGTCGGAGAA	ACGTGGGAGA	AGGCAGCGGA	CGCATCACTT	GCACTTCTAG
401	AAATAGATGC	AACGATCAGG	ACACAAGGAC	ATCCTATAGA	ATTGGAGACA
451	CCTGGAGCAA	GAAGGATAAT	CGAGGAAACC	TGCTCCAGTG	CATCTGCACA
501	GGCAACGGCC	GAGGAGAGTG	GAAGTGTGAG	AGGCACACCT	CTGTGCAGAC
551	CACATCGAGC	GGATCTGGCC	CCTTCACCGA	TGTTCGTATT	GCTGGACCTG
601	AGTGGCTGCT~	AGACCGTCCA	TCTGTCAACA	ACAGCCAATT	GCTTGTTAGC
651	GTTGCTGGTA	CTGTTGAGGG	GACGAATCAA	GACATTAGTC:	TTAAATTTTT
701	TGAAATCGAT	CTAACATCAC	GACCTGCTCA	TGGAGGAAAG	<b>ACAGAGCAAG</b>
<b>751</b>	GCTTAAGTCC	AAAATCAAAA	CCATTTGCTA	CTGATAGTGG ·	CGCGATGTCA
801	CATAAACTTG	AGAAAGCTGA	CTTACTAAAG	GCTATTCAAG -	AACAATTGAT:
851	CGCTAACGTC	CACAGTAACG	ACGACTACTT	TGAGGTCATT	GATTITGCAA
901	GCGATGCAAC	CATTACTGAT	CGAAACGGCA	AGGTCTACTT	TGCTGACAAA
951	GATGGTTCGG	TAACCTTGCC	GACCCAACCT	GTCCAAGAAT	TTTTGCTAAG
1001	CGGACATGTG	CGCGTTAGAC	CATATAAAGA	AAAACCAATA -	CAAAACCAAG
1051	CGAAATCTGT	TGATGTGGAA	TATACTGTAC	AGTTTACTCC	CITAAACCCT
1101	GATGACGATT	TCAGACCAGG	TCTCAAAGAT	ACTAAGCTAT',	TGAAAACACT
1151	AGCTATCGGT	GACACCATCA	CATCTCAAGA	ATTACTAGCT	CAAGCACAAA
1201	GCATTTTAAA	CAAAAACCAC	CCAGGCTATA	CGATTTATGA	ACGTGACTCC
1251	TCAATCGTCA	CTCATGACAA	TGACATTTTC	CGTACGATIT	TACCAATGGA
1301	TCAAGAGTTT	ACTTACCGTG	TTAAAAATCG	GGAACAAGCT	TATAGGATCA
1351	ATAAAAAATC	TGGTCTGAAT	GAAGAAATAA	ACAACACTGA	CCTGATCTCT
1401	GAGAAATATT	ACGTCCTTAA	AAAAGGGGAA	AAGCCGTATG	ATCCCTTTGA
1451	TCGCAGTCAC	TTGAAACTGT	TCACCATCAA	ATACGTTGAT	GTCGATACCA
1501	ACGAATTGCT	AAAAAGTGAG	CAGCTCTTAA	CAGCTAGCGA	ACGTAACTTA
1551	GACTTCAGAG	ATTTATACGA	TCCTCGTGAT	AAGGCTAAAC	TACTCTACAA
1601	CAATCTCGAT	GCTTTTGGTA	TTATGGACTA	TACCTTAACT	GGAAAAGTAG
1651	AGGATAATCA	CGATGACACC	AACCGTATCA	TAACCGTTTA	TATGGGCAAG
1701	CGACCCGAAG	GAGAGAATGC	TAGCTACCAT	TTAGCTGGTG	GTGGCCAGGC
1751	GCAACAGATT	GTACCCATAG	CTGAGAAGTG	TITTGATCAT	GCTGCTGGGA
1801	CTTCCTATGT	GGTCGGAGAA	ACGTGGGAGA	AGCCCTACCA	AGGCTGGATG
1851	ATGGTAGATT	GTACTTGCCT	GGGAGAAGGC	AGCGGACGCA	TCACTTGCAC
1901	TTCTAGAAAT	AGATGCAACG	ATCAGGACAC	AAGGACATCC.	TATAGAATTG
1951	GAGACACCTG	GAGCAAGAAG	GATAATCGAG	GAAACCTGCT	CCAGTGCATC
2001	TGCACAGGCA	ACGGCCGAGG	AGAGTGGAAG	TGTGAGAGGC	ACACCTCTGT
2051	GCAGACCACA	TCGAGCGGAT	CTGGCCCCTT	CACCGATGTT	CGTTAG

Fig. 23



Fraction No.

TEGULES OBETH

Fig. 24

